

Fig. 3-20. Gene expression patterns in response to temperature shift which are different between OLHNI-e1 and OLHdrR-e3 cell lines. OLHNI-e1 and OLHdrR-e3 cell lines from the Northern and Southern Japanese population, respectively, were cultured at 25°C to the confluent, and then transferred to 15°C. Each row represents a single cDNA clone. The name of genes encoded by cDNA clones are shown if the annotation data are available.

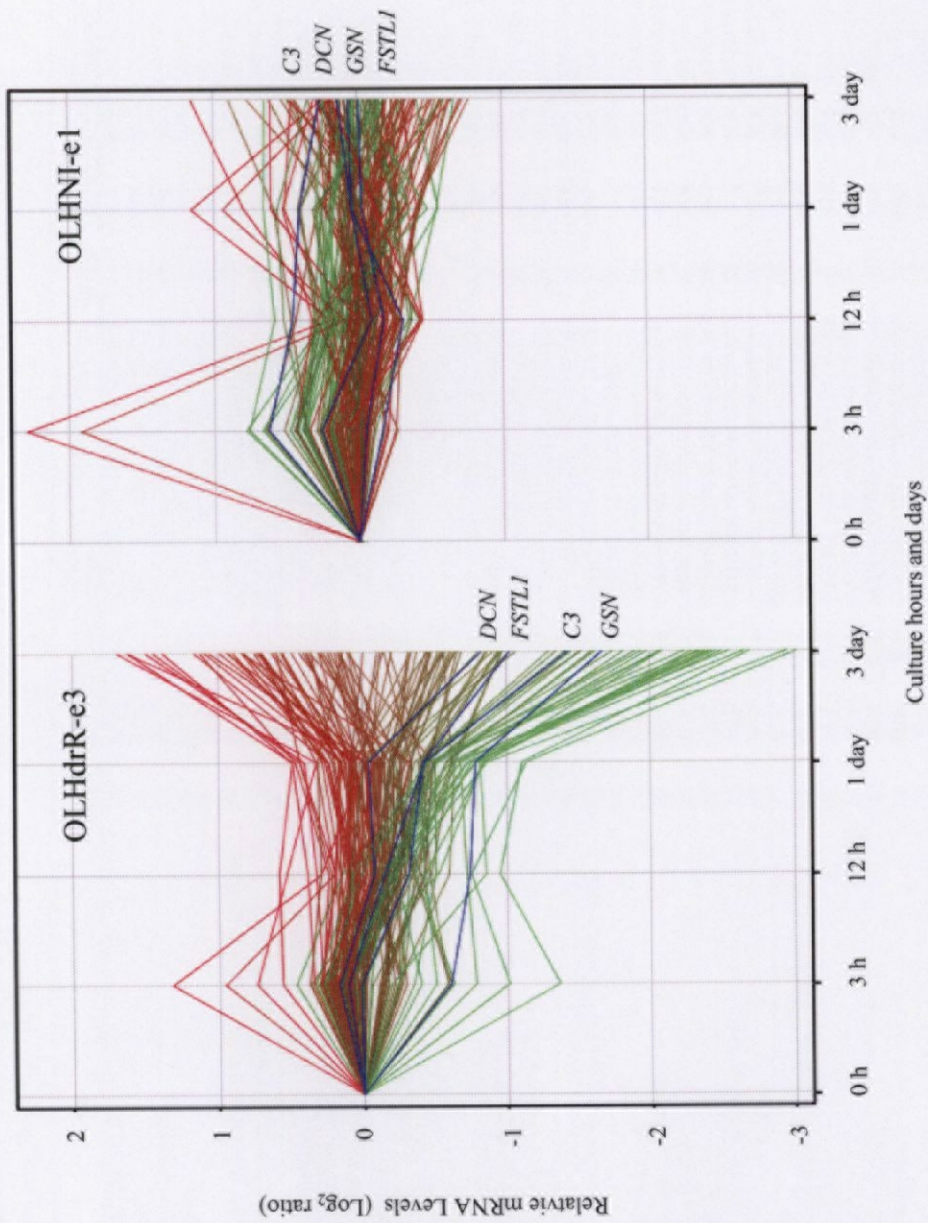


Fig. 3-21. Expression profiles of genes related to extracellular component in OLHNI-e1 and OLHdrR-e3 cell lines during 3 days at 15°C. Lines represent cDNA clones as shown in Fig 3-17. Four genes related to extracellular of cellular component in GO term (see Supplementary Table 3-7) were represented by blue lines. Y-axis and color gradient are determined as shown in Fig. 3-17. C3; complement component 3, DCN; decorin, FSTL1; follistatin-like 1, GSN; gelsolin.

Supplementary Table 1-1. Selected clones encoding the genes related to temperature acclimation and their specific primer pairs used in PCR amplification. Primers were designed using Primer3 program (Rozen and Skaletsky, 2000).

Clone ID	Gene	5' primer			3' primer			No. in Table 1-3		
		Length	T _m (°C)	GC (%)	Sequence	Length	T _m (°C)		GC (%)	Sequence
OLA01.02c	F-actin capping protein beta subunit	25	60.5	44.0	ACAGATCCCCCTGGAGTAATAAGTA	25	60.1	40.0	CTCTGTATGATCAAAAGGGTTAT	1
OLA01.05f	Maltase-glucoamylase	24	60.1	33.3	ATGTAATGAAGTTTGGATGGCCCTT	25	60.5	36.0	CTCTTTTCCCACTCACTGAAATTTG	2
OLA03.05a	Acetyl-coenzyme A acetyltransferase 2	25	60.1	40.0	ATCAACTGAGTCGTGTGAAGTAA	25	60.0	40.0	ATCCTTAAGACTTCTGAAACACAG	3
OLA03.12f	Aspartate aminotransferase 1	22	61.1	54.6	GAGCTTACCCTACCGATGACTG	22	60.7	50.0	AAGGTACTCGTGGTTCAAGCTG	3
OLA06.04e	Hexokinase 2	25	60.0	32.0	GTGGAATGGAAACAAAGATTTATG	25	60.0	40.0	TTCACTCCATAAAGTTAGCAGAAC	4
OLA06.09h	Succinate dehydrogenase complex, subunit A, flavoprotein precursor	25	59.9	32.0	AAGAAATAATCCAAAGTTTTCAGATG	25	59.8	40.0	GATCCCTCACGTGTGTCAATAGAAC	4
OLA07.11h	3-hydroxy-3-methylglutaryl-coenzyme A synthase (soluble)	24	60.9	45.8	GTATCATTCCTGGAGCTGTAAT	24	59.6	41.7	CATTAATCACGCTTTGACAGACTT	5
OLA08.12g	Transketolase	25	59.9	36.0	CAAGTCCAAATAAATCAATGGCTAACT	25	60.1	40.0	ACCAGATCAGACTCTTTGACAAAA	6
OLA22.09f	Protein disulfide isomerase-related protein	25	60.0	36.0	CCATCAAGATCTTTGGAGCTTAATA	25	60.1	36.0	TCTTAATAAAGTTGTTCATCAGTC	7
OLA27.04f	Poly(A) binding protein, cytoplasmic 1 (PABPC1)	25	60.0	40.0	GCTAAAATGTCTTAGACCGTTGAGT	25	59.8	32.0	TTTAATCACGTCAAAAGTTTCATGTT	8
OLA28.11b	Aspartate aminotransferase 2 precursor	25	60.4	44.0	AAACAGCTGGATAAGAGTACTCTTC	25	60.1	44.0	GTCAATGACCGGTATGCTTTGAG	9
OLA29.03e	NADH dehydrogenase subunit 4	25	59.9	36.0	TCCTTAATACTTTTATTTGCGACTG	25	60.0	36.0	GTTCTTTGCTATGTGGTTTTCAG	10
OLA29.05f	Chaperonin containing TCP1, subunit 2 (beta)	22	60.2	40.5	ATCTGGAGCAGATGAGGAAAAA	23	60.1	47.8	CACTCAGAGGATCTTATCCATC	11
OLA02.09f	Alpha 1 type I collagen	22	59.9	45.5	AAAGGAAAGCTGGTGAGAAATG	23	61.4	47.8	CCTTTAGCTCCAGTGTTCCTCAAC	12
OLA04.05e	Delta-6 desaturase	25	60.2	32.0	ACGAAAATTTTAAACGTCAAAAT	25	59.9	36.0	TATGGAATCATCTTTCTCTCTGTC	13
OLA07.01f	F-actin capping protein alpha-2 subunit	25	60.3	32.0	AGTTTCAACGAATTTTCAATGATGT	25	60.2	40.0	CTTAGTGGTCAAACTTGAAGAG	13
OLA07.12b	Mitogen-activated protein kinase 8 interacting protein 3	25	59.9	48.0	CACCTCCAGATATCTTCTCTCAG	25	59.9	36.0	CATGTGCAGAAATGATGAATCTAAC	14
OLA08.06a	Ribosomal protein S4, X-linked X isoform	23	60.5	43.5	ATGCTACAGATTTGAGAAAGACC	24	60.2	50.0	CTTGTACTTAGCTCTCTCCACT	14
OLA16.02f	BCL2-associated athanogene 2	25	59.6	40.0	ATTGACTGATCGGACTACAGAACT	25	60.3	44.0	GTTAAGCTCAACTCTTCCCTTCT	15
OLA16.11h	Ribosomal protein S11	25	60.0	36.0	GAAGGCACTTACATTTGACAGAAAT	25	60.0	40.0	TTAGTCACTTTGAGGACGTTAAAC	16
OLA17.02c	Translocase of outer mitochondrial membrane 20 (yeast) homolog	25	60.5	36.0	CAATTTAGCAACATCTCTTCCGAAAC	25	59.9	36.0	AAAAATAGTGCAGTAACCGACAAA	17
OLA18.01e	HSP10	21	59.7	52.4	AAGTCTCCCTCTCTGTTCCGAC	20	60.3	55.0	AGCACCTTCCCTCGAGACTT	18
OLA21.02h	Lactate dehydrogenase B (LDHB)	24	59.9	41.7	AAGATTTGGGGGATAAAGACTAC	23	59.7	39.1	CTTGAAGACATTTGACGTTCTT	19
OLA22.10g	NADH dehydrogenase subunit 1 (ND1)	25	60.1	40.0	TGAGCTATATTTCAACTCCGTAAGG	25	60.1	32.0	TGTAAAACCTCCCGTAAAAACAAT	20
OLA24.02f	ADP-ribosylation factor-like 1	25	61.1	48.0	GTGGATTTCTCCAGTCTCTTCTC	25	59.9	40.0	AGTCTGTACAGGATTTGGTFTTTC	21
OLA24.03d	Glutathione peroxidase 4	25	59.8	28.0	TTTATGATTTCAATTCGCAACAGACAT	25	59.7	36.0	CGTCAATTTACTGAAACAGATCAA	22
OLA26.03a	Chaperonin containing TCP1, subunit 6A (zeta 1)	25	60.1	40.0	CACATTCATTCAGAAAGTGTGAGAAC	24	60.4	45.8	GTGTTTCACTAGAGCATCTGCAAC	22
OLA26.03a	HSP90	25	59.9	40.0	CTTCCACATTTTAAAGCCTCACTTTC	25	59.7	36.0	CCTACTTTCAAACAAGGTTTFTCA	23
OLA27.09g	Ribosomal protein S10	25	60.6	40.0	TTTTTACTGTTACTGCTCAATTTTA	25	59.8	40.0	ACCTCTAAAGTGGAAATCTGTAGC	24
OLA28.12d	Oxidative stress protein A170	25	60.2	32.0	AACCTCGAATATCATCAGCAAGAAA	25	60.0	36.0	TCTGACGTTATGTTTTAGGTGTTTC	25
OLA29.09h	Ribosomal protein L17	24	60.8	37.5	ATCCTCTTTTTTAAATCTTTCGCTGT	25	60.2	40.0	ACTAAAACCCACTCTTAACCGAAC	26
OLA30.01e	G protein-binding protein CRFG	25	60.0	32.0	AAITTAATGATCATCACCTTATCCAA	25	59.9	40.0	TTAGCTATGTTTTATCTGCCCCAAC	27
OLA32.03c	GrpE-like protein cochaperone	25	60.6	28.0	CAAGAANAATGCCGAAATAACAAA	24	60.2	45.8	CTGATCCCGTATGATTTAGCATC	28
OLA02.11e	Anti-oxidant protein 2	25	59.3	44.0	CTTGTCTATTGACAGTGTGAGGAC	25	60.0	40.0	CAGCTCTCTGTTATCATCAGCAAT	28
OLA03.12c	HSP70	21	59.9	42.9	CGGTTCCAAACACACACTTTT	25	60.7	48.0	ACACAGGATGAGTGGTCTCTAGA	29
OLA10.06g	Translocase of inner mitochondrial membrane 8 (yeast) homolog B	25	60.6	40.0	CCATCCCTGTTTCCACACTTAACTA	25	60.1	32.0	ACAATGACACATGGAAGGAAATAAA	30
OLA11.12a	Capping protein (actin filament), gelsolin-like	24	60.1	45.8	GTGTGTTAGGACGAGTTTCTCT	25	60.1	40.0	GGAAGTTATGTTGGTTGTGTAAA	30
OLA12.09b	Glutathione peroxidase 1	25	60.0	40.0	AAAGTTCTCTCATATAGAAATGTGG	25	60.9	36.0	ATTTCTTCACTTCTGACGTTCTCT	31
OLA12.11e	Myosin regulatory light chain	25	60.0	40.0	CCAGAGTTCCACATCTGAAATAGTTT	25	59.9	32.0	TAAACCTGATTCGATGAGTTTCAT	31

Supplementary Table 1-1. continued

Clone ID	Gene	5' primer			3' primer			No. in Table 1-3		
		Length	T _m (°C)	GC (%)	Sequence	Length	T _m (°C)		GC (%)	Sequence
OLc17.04e	Pyrophosphatase (inorganic)	25	60.0	36.0	AGTTATTCGGATTAAACGGTGAAGAC	25	60.0	36.0	CTATCAACAACAAGTGTGTTTTC	32
OLc25.03c	HSP47	24	60.9	41.7	AATCTGGCCCTTTAACCTTTTACCAC	25	61.2	44.0	GTGTTGATCTCCAGGTAGTGT	33
OLc28.06a	Chaperonin containing TCPI1, subunit 4 (delta)	25	60.6	40.0	CGTAAACCGTTTGCATCTACTATAA	25	60.8	40.0	GTGATGTGCACATCTCCCTTCTCA	
OLc28.09b	Charmine palmitoyltransferase 1	25	60.0	44.0	GGCCTCTGTGAACACATAACAGTAAT	25	60.0	40.0	ACACCCAGTACACACTGTTCTTGA	
OLc29.03e	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa	25	60.0	44.0	TAAACTTCCCTGTAGTCCCAAGTCAC	25	59.7	36.0	CTATTTCTACAAGACAACAACAAAGC	34
OLc32.11h	Ras-related GTP-binding protein 4b	25	59.6	44.0	GTCTGTAACAGTAAACCTTGAAGAG	25	60.0	40.0	ACTTGAACAGTAAACCTTGAAGAG	
OLc33.06h	Protein tyrosine phosphatase, non-receptor type 23	24	60.8	50.0	GAGAGTGAATGGTCCCTTGAGAGAG	25	59.8	40.0	TGCTCTGATAGTCACTGCTTGTTC	35
OLc33.07f	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa	21	60.4	52.4	CAGTTCAGGAACATGGTGGAC	23	60.5	47.8	GTGAGTGTAAACCCAGAGAAAGC	
OLc37.07d	RAS-like protein B	25	60.0	44.0	TACTGGTAAGAACAAGAACCCAGACC	24	60.5	41.7	AACATCATGTACATGAACCTGCAAC	36
OLc37.11d	Stress-activated protein kinase	25	59.6	40.0	TCCATCTACTACATCACTGGTGAATC	25	59.9	44.0	TGGAGACAGTCACTCTCTACTACT	37
OLc50.11d	HSP84	25	59.9	40.0	ACTCAGCAAGTCCAGATACCAACCT	21	60.0	47.6	CGGCCACTTCTATGATGTGAT	
OLc56.05g	Rho GTPase activating protein 1	24	60.6	45.8	GAGCTAAACCGTATGTGAAGAAATC	25	59.9	44.0	ACCATAGTGAAGCATCTTTAGCAAA	38
OLc58.11d	Uroporphyrinogen decarboxylase	23	59.8	47.8	CAGACGTGATCGTTGAGTATCTG	25	60.1	40.0	ACATATGATGAGCATCTTCCAGTGT	39
OLd02.11b	Aldehyde dehydrogenase 9	20	59.6	55.0	AAGAAAGTCTGGCCAGGAG	23	60.5	39.1	CATTTGTTGATCACTTCCAGTGT	40
OLd09.03f	Dyskerin	25	59.9	36.0	TCTCAAGAACTTCGATTAAGCTGAAT	25	59.9	40.0	TTTCTTGAGTGTGTAACCTCTGTC	41
OLd09.06d	Nucleolar protein family A, member 3	25	60.1	28.0	TTACCGATAAACAATCAAGCATTTT	25	59.9	40.0	CAGTCTGCTTTTGGTGGTCTG	42
OLd10.09h	Inhibitor of nuclear factor-κB, alpha (IκBα)	21	62.2	47.6	CTCCACTTGGCCATCATTTT	22	59.8	50.0	GTGTGTAATCCACACAGTGTGTGAG	
OLd12.06e	SLIT-ROBO Rho GTPase-activating protein 3	25	60.1	44.0	CAGCTTATAGCAACCTGAAGTGT	25	60.0	36.0	GCTGTTTTTCAAAATAGAGTGTGT	
OLd23.12h	RNase MRP/RNase P protein-like	25	60.0	24.0	ATGCTAAAGTAGCCCTGTGAGACTGT	25	60.0	36.0	TTATTTTGGATGAAGTTGCCCTAGAG	
OLd27.12h	Stress-induced-phosphoprotein 1	25	59.9	44.0	TGTTTAAATCGGATTCACAATTTT	25	60.1	40.0	ACATATGAGTCTTATAGTCAAAAGC	
OLd32.04h	Methionine adenosyltransferase II, alpha	25	59.9	44.0	AATCAGACCTCTGTGGAGACATTCAC	25	60.1	41.7	ATCCCTTGGATCATCTTTTGAGAG	
OLd32.05e	ADP-ribosylation factor 5	25	60.0	44.0	TAAAGGAGGCTCTCGGAAGTATTTT	25	60.0	40.0	ATPAGCCCAAGTAGGTAATAATGAAC	43
OLd49.11g	Translocase of inner mitochondrial membrane 23 (yeast) homolog	25	59.9	36.0	TACGCTAAATTAGAACCCAGTTGAC	25	60.1	36.0	TTACGAACATGAAGGGAGACATAT	44
OLd52.07h	N-acetyltransferase, homolog of <i>S. cerevisiae</i> ARD1	25	60.0	40.0	TTAGAAGAAATGTCTTGTATGATGG	25	60.2	40.0	CAFTCAAGAAGTCACTCTCTTCT	
OLd55.03g	Translocase of inner mitochondrial membrane 10 homolog (yeast) (TIM)	25	59.6	36.0	AAAGACTACACCCTCTGTTTCAAGC	24	60.0	50.0	GTGTTCCCTGTPAGTACGTTGGAAGTG	45
OLd57.04g	Ras-related protein Rab-1c	25	60.1	40.0	CAAGTTTCAGGATGTTATGTTT	25	60.1	40.0	GTAGGATTCCTTGAACAAACTCTC	46
OLd57.09h	Spermidine synthase	25	59.7	32.0	GAGTACCTGGACCTTACTCTCATC	25	60.0	44.0	GCCCATGTTAGTCTTGTAGTCTATG	47
OLd58.11f	Aldo-keto reductase family 1, member A1	24	59.6	54.2	ATAAATACAGGAGCAATGCTGAAG	25	59.8	48.0	GAGTAGATCCCTGGAAAGTCTCTC	48
OLd59.03d	COP9 homolog	25	60.1	36.0	AACATTTTCTCCACTCAGGATCAC	25	59.8	36.0	ABCTAGATACCAGAAAGCGAAC	49
OLd61.07d	S-adenosylhomocysteine hydrolase; adenosylhomocysteinase	24	60.8	41.7	CTGGAAGACCCAGTATGAGATCAAT	25	59.8	48.0	AGAGTTTCAGACGTCCTCCATACAGTAG	
OLd69.02e	Ras-related GTP-binding protein RAGA	25	60.0	44.0	CAGCATTCAGAACTTCTTCTACTCC	25	60.1	48.0	AGAGTTTCAGACGTCCTCCATACAGTAG	
OLd71.04f	S-adenosylmethionine decarboxylase 1 precursor	25	60.1	36.0	TTTGTCTACAGAGAACAAGGTTACA	25	60.2	36.0	GCCAAAATCTTTATTCATCTCTCC	50
OLd76.05c	Guanine monophosphate synthetase	25	60.5	44.0	ACAGTCTGAAGAAGTCAAGAAAG	25	59.2	36.0	AAATATTTAGTCTAGCGTTTTTCCA	
OLd77.12e	Ribosomal protein L24	25	59.9	48.0	GGGTTAGTGTACTACCTGACAGA	25	60.3	36.0	GTTTGTTTTTAGCTTTGTGAACAC	51
OLd79.06g	Cyclin-dependent kinase 2, isoform 1	25	59.6	32.0	ATCAAAAGCATCAACTTAGAGAAAT	25	59.9	40.0	CTTTTACCAAGAGAGGGTGTAAAT	
OLd80.12c	Oxidative-stress responsive 1	25	60.1	40.0	ATCTCTCAACACAGAACAAAGGTGAC	25	60.0	40.0	TAGCTGCTTTTTCACCCAAAGATAT	
OLe05.07h	Dihydroliipoamide dehydrogenase precursor	25	59.8	36.0	ACTAAAGATCAACCCAGGCTAAAAT	25	60.2	44.0	CTTCTCAATGGTAGTAACACACACC	
OLe13.03f	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	25	60.3	28.0	TTTTTCTGTTTTGGCATTTTGTACT	25	60.3	40.0	TAAAGCTTTTATGTTCTTCTGTCG	
OLe13.06h	HSP40	25	59.9	36.0	GTTTCAGCATCTCTCTGTTAAAGATAA	25	60.0	36.0	ATGAAATCCCTCTCTTTTCTTACT	
OLe14.07g	Glutamate decarboxylase 1 isoform GAD67	25	59.9	36.0	GTTTCAGCATCTCTCTGTTAAAGATAA	25	60.0	36.0	ATGAAATCCCTCTCTTTTCTTACT	

Supplementary Table 1-1. continued

Clone ID	Gene	5' primer			3' primer			No. in Table 1-3		
		Length	T _m (°C)	GC (%)	Sequence	Length	T _m (°C)		GC (%)	Sequence
OLe15.05e	Cell division cycle 42 isoform 2	25	60.0	40.0	AACAGAGCGTCTTCCTGTGTATGTTTC	25	60.0	40.0	AGCTTCTCAATAGTGTGTGTGTCT	52
OLe17.08b	Chaperonin containing TCP1, subunit 8 (theta)	25	59.9	40.0	TAGAAGGGAGCTTTCGTGPAACAT	25	60.0	36.0	TCGTTGGCCATCTGTTTACTCATA	53
OLe18.04a	Dihydropyrimidinase	25	59.6	40.0	CCCTCAATGTCAGAAATAGCTTTAAC	25	60.1	40.0	AGAAAACACACAGACACACAAAG	54
OLe20.05b	Transferrin	25	60.9	40.0	AGAAAGAAAGACCCCTTGACTGTAT	25	60.0	44.0	GGTCAATAGTTGTTAAGACCAGCAGT	
OLe20.08h	Ependymin	25	60.0	40.0	CTCTCTGTGAACACTCAAAATGAGA	25	59.9	40.0	GTTGATCTTGTACAGAACACCCCTTT	
OLf01.04f	Chaperonin containing TCP1, subunit 3 (gamma)	25	59.9	44.0	ACCGTGAATATTAGTGCCTACAGAC	25	60.1	36.0	CGTAGTCTTGTATGTCGATTTCTT	55
OLf01.11e	δ-aminolevulinic acid dehydratase (ALAD)	24	60.5	45.8	CTCAGACCCGAGAAATCTCAITTTAC	23	59.8	39.1	CAAAGATCAGCACACATTTCAAG	56
OLf02.04f	Tumor rejection antigen gp96	23	59.5	43.5	ATTGAAGATCACTCCAACAGGAC	25	60.2	40.0	AAATAGTCTTGTCTCTCTCTCTCT	57
OLf23.05e	Succinate dehydrogenase complex, subunit D precursor (SDHD)	25	60.5	48.0	GATTTGACAGGTTCTCACAGACTAC	25	59.4	36.0	TAGTTGAAGTAAACAAGACCAGCA	58
OLf28.09g	Mitogen-activated protein kinase 1 interacting protein 1	23	60.9	43.5	GTAATCAAAAGTTCCACAGCAG	25	60.0	40.0	AGTAGCAGATGATGCTCTTGTCTT	59
OLf29.07c	Annexin V	25	59.5	36.0	AAAGACTGTTAAATGGTTCAGAAAG	25	60.0	40.0	TATCAGATCTCTTCCAAACAGAGT	60
OLf29.09h	Glutamate dehydrogenase 1	25	60.0	44.0	ACTCAAACTACCACCTTCTCATGTC	25	59.9	44.0	CGTTGTAGACTTTGAAGACCTTCT	61
OLf42.04b	Fibrillarin	23	59.4	43.5	AGACATGAAGGGGTGTTTATCTG	25	59.8	44.0	ACTCAATCTTAGGTATCACCCCTCT	
OLf42.12h	Phosphatidic acid phosphatase type 2B	19	62.9	57.9	GGCATTGTTTATTACGTTTCAGACC	22	60.9	50.0	GGTTGTTCTCTCGATGATGTC	62
OLf48.01e	Ferritin H	20	63.8	50.0	TCCTCCACTTTCATGACGACG	23	61.2	43.5	AAATCCTRAAGTCTCATAGTCCG	63
OLb07.07a	COXII	20	59.4	45.0	CACAGCATTTCTCATCAGTTG	21	63.6	57.1	GGACAGCAGACAGTAGGTTGG	64
OLb07.11b	Cytochrome b	22	62.4	45.5	CTGAAGTCCATCAAGAATCC	21	63.1	47.6	TCCTCGCTCTTTATGACCTTGG	65
OLb16.07f	γ-F ₁ -ATPase	20	61.4	50.0	CTTTCCAGACCAGTTTCAGC	20	59.4	45.0	CATAAGAGAAAAGCTGCTGC	66
OLc02.10h	c-F ₁ -ATPase	20	62.3	55.0	GAGACGGTATTGTCAGAGTG	20	63.0	50.0	ATGGCATTTCTTAGAGCGTC	67
OLe13.07b	α-F ₁ -ATPase	24	75.3	62.5	CACCTCAGCCCGCTCACACACAG	24	82.0	70.8	TGACACCCCTGGTGCCTGGGGCGAC	68
OLa06.08f	β-actin	22	73.3	63.6	GGAGCCAGGCACAAAGATGAGC	22	73.6	63.6	ACACGGCCAGCAGAGTCTC	69
OLa27.09c	EF-1α	25	60.1	36.0	CTTCTTCTTGGACAAACAAGTGTTC	25	60.1	32.0	AGAAATGGGAAGATTTCTGCTCTTTT	70
OLa22.08f	mWap65-1	25	60.2	40.0	CAACCATCCAGTCAGTATTTTAAAGG	25	60.0	40.0	CATCTTTGGGATAAATPACCAGTCA	71

Supplementary Table 1-2. Medaka candidate genes analyzed by RT-PCR and possibly to change their expression levels in a temperature-dependent manner

No.	Clone ID	Gene	No.	Clone ID	Gene
1	OLa01.02c	F-actin capping protein beta subunit	37	OLc50.11d	HSP84
2	OLa03.05a	Acetyl-Coenzyme A acetyltransferase 2	38	OLc58.11d	Uroporphyrinogen decarboxylase
3	OLa03.12f	Aspartate aminotransferase 1	39	OLd02.11b	Aldehyde dehydrogenase 9
4	OLa06.09h	Succinate dehydrogenase complex, subunit A, flavoprotein precursor	40	OLd09.03f	Dyskerin
5	OLa07.11h	3-Hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	41	OLd09.06d	Nucleolar protein family A, member 3
6	OLa08.12g	Transketolase	42*	OLd10.09h	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (I κ B α)
7	OLa22.09f	Protein disulfide isomerase-related protein	43	OLd52.07h	<i>N</i> -acetyltransferase, homolog of <i>S. cerevisiae</i> ARD1
8*	OLa27.04f	Poly(A) binding protein, cytoplasmic 1 (PABPC1)	44*	OLd55.03g	Translocase of inner mitochondrial membrane 10 homolog (yeast) (TIM10)
9	OLa28.11b	Aspartate aminotransferase 2 precursor	45*	OLd57.04g	Ras-related protein Rab-1c
10	OLa29.03e	NADH dehydrogenase subunit 4	46*	OLd57.09h	Spermidine synthase
11	OLa29.05f	Chaperonin containing TCP1, subunit 2 (beta)	47	OLd58.11f	Aldo-keto reductase family 1, member A1
12	OLb02.09f	Alpha 1 type I collagen	48*	OLd59.03d	COP9 homolog
13	OLb07.01f	F-actin capping protein alpha-2 subunit	49	OLd69.02e	Ras-related GTP-binding protein RAGA
14	OLb08.06a	Ribosomal protein S4, X-linked X isoform	50	OLd77.12e	Ribosomal protein L24
15	OLb16.02f	BCL2-associated athanogene 2	51	OLd80.12c	Oxidative-stress responsive 1
16	OLb16.11h	Ribosomal protein S11	52	OLe15.05e	Cell division cycle 42 isoform 2
17	OLb17.02c	Translocase of outer mitochondrial membrane 20 (yeast) homolog	53	OLe17.08b	Chaperonin containing TCP1, subunit 8 (theta)
18	OLb18.01e	HSP10	54	OLe18.04a	Dihydroliipoamide S-acetyltransferase
19*	OLb21.02h	Lactate dehydrogenase B (LDHB)	55	OLf01.04f	Chaperonin containing TCP1, subunit 3 (gamma)
20*	OLb22.10g	NADH dehydrogenase subunit 1 (ND1)	56*	OLf01.11e	δ -Aminolevulinic acid dehydratase (ALAD)
21	OLb24.03d	Glutathione peroxidase 4; phospholipid hydroperoxidase	57*	OLf02.04f	Tumor rejection antigen gp96
22	OLb26.03a	Chaperonin containing TCP1, subunit 6A (zeta 1)	58*	OLf23.05c	Succinate dehydrogenase complex, subunit D precursor (SDHD)
23	OLb26.05a	HSP90	59	OLf28.09g	Mitogen-activated protein kinase kinase 1 interacting protein 1
24	OLb27.09g	Ribosomal protein S10	60	OLf29.07c	Annexin V
25	OLb28.09e	Peptidylprolyl isomerase-like protein 3 isoform PPIL3b	61	OLf29.09h	Glutamate dehydrogenase 1
26	OLb28.12d	Oxidative stress protein A170	62	OLf48.01e	Ferritin H
27	OLb30.01e	G protein-binding protein CRFG	63	OLb07.07a	COXII
28	OLc02.11e	Anti-oxidant protein 2	64	OLb07.11b	Cytochrome b
29	OLc03.12c	HSP70	65	OLb16.07f	Gamma-F1-ATPase
30	OLe11.12a	Capping protein (actin filament), gelsolin-like	66	OLc02.10h	c-Fo-ATPase
31	OLc12.11e	Myosin regulatory light chain	67*	OLe13.07b	α -F ₁ -ATPase
32*	OLc25.03c	HSP47	68	OLa06.08f	β -actin
33	OLc28.06a	Chaperonin containing TCP1, subunit 4 (delta)	69	OLa27.09c	EF-1 α
34	OLc29.03e	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa	70	OLa22.08f	mWap65-1
35	OLc33.07f	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa	71	OLe19.09a	mWap65-2
36	OLc37.11d	Stress-activated protein kinase			

*Upregulation (No. 8, 19, 20, 42, 44, 45, 46, 48, 56, 57, 58 and 67) and downregulation (No. 32) upon the shift of incubation temperature from 33 to 25°C were demonstrated by RT-PCR analysis (See Fig. 1-5)

Supplementary Table 2-1. Gene Ontology terms and numbers of cDNA clones in medaka OL libraries

GO term	All		OLb		OLc		OLd		OLe		OLf	
	Number of clones GO term	Number of clones in GO term	Number of clones GO term	Number of clones in GO term	Number of clones GO term	Number of clones in GO term	Number of clones GO term	Number of clones in GO term	Number of clones GO term	Number of clones in GO term	Number of clones GO term	Number of clones in GO term
All	3840	1476	1233	642	268	99	1549	577	325	121	174	37
Molecular function	1331	573	525	110	110	110	525	40	12	12	34	6
Signal transducer activity	122	53	11	11	11	11	40	21	5	5	2	2
Receptor activity	55	25	2	2	2	2	21	10	6	6	2	2
Receptor binding	42	19	5	5	5	5	10	5	5	5	3	3
Receptor signaling protein activity	15	5	2	2	2	2	5	331	62	62	23	23
Binding	832	361	55	55	55	55	331	1	1	1	1	1
Amino acid binding	3	1	1	1	1	1	1	1	1	1	1	1
Calcium oxalate binding	1	1	1	1	1	1	1	1	1	1	1	1
Calcium oxalate binding	7	5	5	5	5	5	5	1	1	1	1	1
Carbohydrate binding	5	2	2	2	2	2	3	3	3	3	3	3
Cofactor binding	5	5	4	4	4	4	4	1	1	1	1	1
Drug binding	14	8	8	8	8	8	1	1	3	3	1	1
Glycosaminoglycan binding	4	2	2	2	2	2	2	9	4	4	3	3
Isoprenoid binding	33	15	2	2	2	2	15	86	24	24	9	9
Lipid binding	199	65	15	15	15	15	86	121	14	14	6	6
Metal ion binding	300	140	19	19	19	19	121	96	11	11	3	3
Nucleic acid binding	220	92	18	18	18	18	96	1	1	1	1	1
Nucleotide binding	3	2	2	2	2	2	2	1	1	1	1	1
Oxygen binding	8	6	6	6	6	6	6	96	12	12	11	11
Peptide binding	232	98	98	98	98	98	96	1	1	1	1	1
Protein binding	1	1	1	1	1	1	1	10	6	6	2	2
Pyridoxal phosphate binding	42	19	19	19	19	19	5	1	1	1	1	1
Receptor binding	1	1	1	1	1	1	1	3	3	3	3	3
Ribonucleoprotein binding	3	3	3	3	3	3	3	2	2	2	2	2
Selenium binding	4	4	4	4	4	4	4	1	1	1	1	1
Steroid binding	6	3	3	3	3	3	3	2	2	2	2	2
Tetrapyrrole binding	4	4	4	4	4	4	4	1	1	1	1	1
Vitamin binding	591	221	41	41	41	41	244	72	72	72	13	13
Catalytic activity	11	4	4	4	4	4	5	2	2	2	2	2
Helicase activity	232	86	11	11	11	11	103	30	30	30	2	2
Hydrolase activity	33	22	22	22	22	22	10	1	1	1	1	1
Isomerase activity	64	21	3	3	3	3	31	8	8	8	1	1
Kinase activity	54	17	6	6	6	6	27	3	3	3	1	1
Ligase activity	28	6	2	2	2	2	15	5	5	5	5	5
Lyase activity	120	55	16	16	16	16	32	12	12	12	5	5
Oxidoreductase activity	1	1	1	1	1	1	1	8	8	8	5	5
Polyketide synthase activity	13	4	4	4	4	4	8	24	24	24	5	5
Small protein conjugating enzyme activity	151	43	28	28	28	28	69	16	16	16	9	9
Transferase activity	58	28	28	28	28	28	5	9	9	9	5	5
Enzyme regulator activity	1	1	1	1	1	1	1	4	4	4	1	1
Caspase regulator activity	15	8	8	8	8	8	3	4	4	4	8	8
Enzyme activator activity	31	13	13	13	13	13	2	8	8	8	2	2
Enzyme inhibitor activity	16	6	6	6	6	6	7	7	7	7	7	7
GTPase regulator activity	2	2	2	2	2	2	2	2	2	2	2	2
Nitric-oxide synthase regulator activity	5	5	5	5	5	5	3	3	3	3	3	3
Kinase regulator activity	2	2	2	2	2	2	2	2	2	2	2	2
Ornithine decarboxylase regulator activity	2	2	2	2	2	2	1	1	1	1	1	1
Phosphatase regulator activity	3	3	3	3	3	3	3	3	3	3	3	3

Supplementary Table 2-1. continued

GO term	All		OLb		OLc		OLd		OLe		OLf	
	Number of clones	Number of clones in GO term	Number of clones	Number of clones in GO term	Number of clones	Number of clones in GO term	Number of clones	Number of clones in GO term	Number of clones	Number of clones in GO term	Number of clones	Number of clones in GO term
	3840	1476	1233	642	268	99	1549	577	325	121	174	37
Molecular function	1331	573	573	74	11	89	525	57	110	34	7	7
Transporter activity	166	74	74	2	1	11	57	1	17	7	7	7
Amine/polyamine transporter activity	3	2	2	1	1	1	2	1	1	1	1	1
Auxiliary transport protein activity	5	1	1	1	1	1	2	2	1	1	1	1
Carbohydrate transporter activity	2	1	1	1	1	1	2	2	1	1	1	1
Carrier activity	65	32	32	6	2	7	21	21	4	4	1	1
Channel/pore class transporter activity	13	6	6	1	1	2	5	5				
Drug transporter activity	1	1	1	1	1	1	1	1				
Electron transporter activity	48	23	23	3	3	3	15	15	5	5	2	2
Intracellular transporter activity	3	2	2	2	2	1	1	1				
Ion transporter activity	53	27	27	7	7	7	14	14	4	4	1	1
Lipid transporter activity	7	1	1	1	1	1	2	2	4	4	1	1
Nucleobase, nucleoside, nucleotide and nucleic acid transporter activity	2	2	2	2	2	1	1	1				
Organic acid transporter activity	3	2	2	2	2	2	2	2				
Oxygen transporter activity	2	2	2	2	2	2	2	2				
Protein transporter activity	16	9	9	9	9	6	6	6				
Vitamin/cofactor transporter activity	1	1	1	1	1	1	1	1				
Transcription regulator activity	92	40	40	40	40	6	43	43	1	1	1	1
Transcription regulator activity	26	12	12	12	12	3	10	10				
RNA polymerase II transcription factor activity	2	2	2	2	2	1	2	2				
RNA polymerase III transcription factor activity	22	6	6	6	6	1	15	15				
Transcription cofactor activity	56	26	26	26	26	2	25	25				
Transcription factor activity	8	2	2	2	2	1	4	4				
Transcriptional activator activity	4	3	3	3	3	1	1	1				
Transcriptional repressor activity	3	3	3	3	3	3	3	3				
Transcription initiation factor activity	1	1	1	1	1	1	1	1				
Transcription termination factor activity	142	92	92	92	92	7	34	34				
Structural molecule activity	11	7	7	7	7	7	7	7				
Extracellular matrix structural constituent	11	7	7	7	7	7	7	7				
Structural constituent of bone	2	2	2	2	2	2	2	2				
Structural constituent of cytoskeleton	14	5	5	5	5	7	7	7				
Structural constituent of muscle	3	1	1	1	1	1	2	2				
Structural constituent of ribosome	85	65	65	65	65	5	12	12				
Translation regulator activity	40	20	20	20	20	3	13	13				
Translation factor activity, nucleic acid binding	40	20	20	20	20	3	13	13				
Chaperone regulator activity	1	1	1	1	1	1	1	1				
Antioxidant activity	7	4	4	4	4	1	2	2				
Chaperone regulator activity	6	4	4	4	4	1	1	1				
Peroxidase activity	39	12	12	12	12	4	19	19				
Molecular function unknown	14	5	5	5	5	8	8	8				
Motor activity	14	2	2	2	2	4	4	4				
Microtubule motor activity	14	2	2	2	2	4	4	4				

Supplementary Table 2-1. continued

GO term	All		OLb		OLc		OLd		OLe		OLf	
	Number of clones	Number of clones in GO term	Number of clones	Number of clones in GO term	Number of clones	Number of clones in GO term	Number of clones	Number of clones in GO term	Number of clones	Number of clones in GO term	Number of clones	Number of clones in GO term
All	3840	1476	1233	642	268	99	1549	577	325	121	174	37
Biological process		1294		565		85	494		50		32	
Cellular process		597		253		42	234		19		18	
Cell communication		221		100		18	75		5		1	
Cell differentiation		476		195		35	190		41		15	
Cellular physiological process		7		3		3	3		1		1	
Membrane fusion		89		34		8	31		11		5	
Regulation of cellular process		1181		510		77	457		106		31	
Physiological process		476		195		35	190		41		15	
Cellular physiological process		18		2		2	5		10		1	
Coagulation		39		15		2	15		6		1	
Death		10		2		1	4		2		1	
Homeostasis		923		415		56	352		83		17	
Metabolism		108		35		6	32		31		4	
Organismal physiological process		4		1		1	1		2		2	
Pathogenesis		176		78		10	69		14		5	
Regulation of physiological process		147		67		5	41		29		5	
Response to stimulus		6		1		1	4		4		7	
Secretion		28		11		2	11		12		1	
Biological process unknown		149		71		11	48		4		1	
Development		2		1		3	5		1		1	
Aging		2		1		1	1		1		1	
Cell differentiation		2		1		1	1		1		1	
Embryonic development		1		1		1	1		1		1	
Genetic transfer		22		8		4	7		1		2	
Growth		104		58		7	28		5		6	
Mesoderm development		3		2		2	2		1		1	
Morphogenesis		1		1		1	1		1		1	
Pattern specification		5		1		1	2		1		2	
Pigmentation		16		5		1	7		1		2	
Regulation of development		3		1		1	1		1		1	
Regulation of gene expression , epigenetic		18		4		1	10		4		1	
Reproduction		1		1		1	1		1		1	
Sex determination		1		1		1	1		1		1	
Sex differentiation		245		106		17	94		18		10	
Regulation of biological process		89		34		8	31		11		5	
Regulation of cellular process		16		5		1	7		1		2	
Regulation of development		9		2		2	5		5		6	
Regulation of enzyme activity		3		1		1	1		1		1	
Regulation of gene expression , epigenetic		176		78		10	69		14		5	
Regulation of physiological process		5		2		2	2		2		1	
Behavior		1		1		1	1		1		1	
Feeding behavior		1		1		1	1		1		1	
Learning and/or memory		2		2		2	2		2		2	
Mechanosensory behavior		3		1		1	2		1		2	
Viral life cycle		3		1		3	1		2		2	
Viral infectious cycle												

Supplementary Table 2-1. continued

GO term	All		OLb		OLc		OLd		OLe		OLf	
	Number of clones GO term	Number of clones	Number of clones GO term	Number of clones	Number of clones GO term	Number of clones	Number of clones GO term	Number of clones	Number of clones GO term	Number of clones	Number of clones GO term	Number of clones
All	3840	1476	1233	642	268	99	1549	577	325	121	174	37
Cellular component		1153	526	489	72	432	396	94	29	26		
Cell		1051	489	44	6	22	71	7	3			
Cell fraction		82	1	1								
Cell projection		1	1									
Intracellular		893	418	1			341	51	21			
Membrane		348	158	1			122	31	13			
Extracellular		108	43	4			26	30	5			
Extracellular matrix		48	27	2			10	8	1			
Extracellular space		34	10	10			10	11	1			
Unlocalized		8	4	4			1	2	1			
cAMP-dependent protein kinase complex		1	1	1								
Ferritin complex		2	1	1								
Glycerol-3-phosphate dehydrogenase complex		1	1	1								
Protein kinase CK2 complex		1	1	1								
Protein serine/threonine phosphatase complex		2	1	1								
Ribonucleoside-diphosphate reductase complex		1	1	1								
Cellular component unknown		38	13	2	2	19	4					

Supplementary Table 2-2. Medaka cDNA clones shown in Figs. 2-2 and 2-3

No.	Clone	Gene
1	OLb28.10h	F-actin capping protein beta subunit
2	OLc18.02g	Aspartate aminotransferase 1
3	OLe12.09g	mWap65-1
4	OLe06.11c	EF-1 α
5	OLc31.12h	Aspartate aminotransferase 2 precursor
6	OLb26.01a	NADH dehydrogenase subunit 4
7	OLd52.11f	Chaperonin containing TCP1, subunit 2 (beta)
8	OLb02.09f	Alpha 1 type I collagen
9	OLb04.05e	Delta-6 desaturase
10	OLb07.01f	F-actin capping protein alpha-2 subunit
11	OLb07.07a	COXII
12	OLb07.11b	Cytochrome <i>b</i>
13	OLb07.12b	Mitogen-activated protein kinase 8 interacting protein 3
14	OLb08.06a	Ribosomal protein S4, X-linked X isoform
15	OLb17.02c	Translocase of outer mitochondrial membrane 20 (yeast) homolog
16	OLb18.01e	HSP10
17	OLb21.02h	Lactate dehydrogenase B
18	OLb22.10g	NADH dehydrogenase subunit 1
19	OLb24.02f	ADP-ribosylation factor-like 1
20	OLb24.03d	Glutathione peroxidase 4; phospholipid hydroperoxidase
21	OLb26.03a	Chaperonin containing TCP1, subunit 6A (zeta 1)
22	OLb26.05a	HSP90
23	OLb27.09g	Ribosomal protein S10
24	OLb32.03c	GrpE-like protein cochaperone
25	OLc12.09b	Glutathione peroxidase 1
26	OLd09.06d	Nucleolar protein family A, member 3
27	OLd12.06e	SLIT-ROBO Rho GTPase-activating protein 3
28	OLd23.12h	RNase MRP/RNase P protein-like
29	OLd49.11g	Translocase of inner mitochondrial membrane 23 (yeast) homolog
30	OLd52.07h	<i>N</i> -Acetyltransferase, homolog of <i>S. cerevisiae</i> ARD1
31	OLd57.09h	Spermidine synthase
32	OLd77.12e	Ribosomal protein L24
33	OLd79.06g	Cyclin-dependent kinase 2, isoform 1
34	OLd80.12c	Oxidative-stress responsive 1
35	OLe05.07h	Dihydrolipoamide dehydrogenase precursor
36	OLb05.04f	Translocase of inner mitochondrial membrane 8 (yeast) homolog B
37	OLb11.02c	HSP47
38	OLb11.03c	ADP-ribosylation factor 5
39	OLb12.12d	HSP108
40	OLb18.08b	Capping protein (actin filament), gelsolin-like
41	OLb26.02b	Dihydrolipoamide dehydrogenase
42	OLb27.10a	Annexin V
43	OLb29.06d	Glutamate dehydrogenase 1
44	OLd65.07c	Stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)
45	OLd74.03f	Methionine adenosyltransferase II, alpha
46	OLb06.08f	β -actin
47	OLb16.02f	BCL2-associated athanogene 2
48	OLb28.09c	Peptidylprolyl isomerase-like protein 3 isoform PPIL3b

Supplementary Table 3-1. Gene Ontology terms and number of clones expressing changes in the accumulated mRNA levels in OLNHN1-e1 cells cultured at 25°C during 7 days

GO term	All				$P < 0.05$			
	Number of clones in GO term	Number of clones in GO term	Expectation	P	Number of clones in GO term	Number of clones in GO term	Expectation	P
All	1353	263	141	135.1	33	20	17.0	33
Molecular function	695	141	135.1	0.422	33	20	17.0	18
Signal transducer activity	624	129	121.3	0.422	19	19	15.2	300
Receptor activity	55	12	10.7	0.599	4	4	1.3	0.344
Receptor binding	22	4	4.3	0.633	6	6	0.5	0.896
Receptor signaling protein activity	20	6	3.9	0.347	1	1	0.5	0.544
Binding	5	1	1.0	0.505	83	83	9.6	0.215
Amino acid binding	395	83	76.8	0.423	12	12	9.6	0.393
Calcium oxalate binding	5	1	1.0	0.505	1	1	0.1	0.215
Carbohydrate binding	4	1	0.8	0.575	1	1	0.1	0.154
Cofactor binding	1	1	0.2	0.404	1	1	0.0	0.002
Drug binding	7	3	1.4	0.279	2	2	0.2	0.001
Glycosaminoglycan binding	19	2	0.4	0.619	1	1	0.0	0.033
Lipid binding	3	3	3.7	0.635	1	1	0.5	0.543
Metal ion binding	72	18	14.0	0.296	5	5	1.8	0.031
Nucleic acid binding	160	30	31.1	0.633	5	5	3.9	0.498
Nucleotide binding	109	21	21.2	0.639	2	2	2.7	0.539
Oxygen binding	1	1	0.2	0.404	1	1	0.0	0.002
Peptide binding	4	1	0.8	0.575	1	1	0.1	0.154
Protein binding	101	27	19.6	0.106	1	1	2.5	0.388
Pyridoxal phosphate binding	20	6	3.9	0.347	1	1	0.5	0.544
Receptor binding	1	1	0.2	0.404	1	1	0.0	0.002
Ribonucleoprotein binding	2	2	0.4	0.619	1	1	0.0	0.033
Selenium binding	2	1	0.4	0.619	1	1	0.0	0.041
Steroid binding	3	3	0.6	0.633	1	1	0.1	0.091
Tetrapyrrole binding	236	62	45.9	0.039	10	10	5.8	0.094
Vitamin binding	4	4	0.8	0.575	1	1	0.1	0.154
Catalytic activity	92	24	17.9	0.159	4	4	2.2	0.301
Helicase activity	12	5	2.3	0.135	1	1	0.3	0.473
Hydrolase activity	21	5	4.1	0.611	2	2	0.5	0.132
Isomerase activity	20	5	3.9	0.576	5	5	0.5	0.544
Kinase activity	11	5	2.1	0.093	2	2	0.3	0.451
Ligase activity	65	17	12.6	0.237	2	2	1.6	0.542
Oxidoreductase activity	1	1	0.2	0.404	1	1	0.0	0.002
Polyketide synthase activity	6	2	1.2	0.577	2	2	0.1	0.269
Small protein conjugating enzyme activity	45	8	8.7	0.637	2	2	1.1	0.473
Transferase activity	22	6	4.3	0.452	2	2	0.5	0.148
Enzyme regulator activity	7	3	1.4	0.279	1	1	0.2	0.317
Caspase regulator activity	12	3	2.3	0.633	2	2	0.3	0.021
Enzyme activator activity	5	1	1.0	0.505	1	1	0.1	0.215
Enzyme inhibitor activity	4	2	0.8	0.346	1	1	0.1	0.154
GTPase regulator activity	1	1	0.2	0.404	1	1	0.0	0.002
Nitric-oxide synthase regulator activity	4	2	0.8	0.346	1	1	0.1	0.154
Kinase regulator activity	1	1	0.2	0.404	1	1	0.0	0.002
Ornithine decarboxylase regulator activity	2	2	0.4	0.619	1	1	0.0	0.033
Phosphatase regulator activity	2	2	0.4	0.619	1	1	0.0	0.033

P and P values were obtained by Kruskal-Wallis ANOVA and χ^2 test, respectively.

Red and blue color boxes represent the clone numbers of which were significantly more and less than the expectation values, respectively ($P < 0.05$).

Supplementary Table 3-1. continued

GO term	All				$P < 0.05$			
	Number of clones GO term	Number of clones in GO term	Expectation	P	Number of clones GO term	Number of clones in GO term	Expectation	P
All	1353	263	141	135.1	33	20	17.0	33
Molecular function	695	129	121.3	0.422	33	20	17.0	18
Transporter activity	624	15	18.3	0.425	2	19	15.2	16
Amine/polyamine transporter activity	1	4	0.8	0.575	0.0	2	2.3	1
Auxiliary transport protein activity	1	1	0.2	0.404	0.0	0.0	0.0	0.0
Carbohydrate transporter activity	1	4	0.8	0.575	0.0	0.0	0.1	0.196
Carrier activity	38	5	7.4	0.404	0.0	0.0	0.0	0.0
Channel/pore class transporter activity	9	1	1.7	0.292	0.9	0.9	0.9	0.9
Drug transporter activity	26	9	5.1	0.109	0.2	0.2	0.2	0.2
Electron transporter activity	3	3	0.6	0.633	0.6	0.6	0.6	0.6
Intracellular transporter activity	37	5	7.2	0.433	0.1	0.1	0.1	0.1
Ion transporter activity	3	3	0.6	0.633	0.9	0.9	0.9	0.9
Lipid transporter activity	2	1	0.4	0.619	0.1	0.1	0.1	0.1
Nucleobase, nucleoside, nucleotide and nucleic acid transporter activity	1	1	0.4	0.619	0.0	0.0	0.0	0.0
Organic acid transporter activity	1	1	0.2	0.404	0.0	0.0	0.0	0.0
Oxygen transporter activity	2	2	0.4	0.619	0.0	0.0	0.0	0.0
Protein transporter activity	8	1	1.6	0.641	0.2	0.2	0.2	0.2
Vitamin/cofactor transporter activity	1	1	0.2	0.404	0.0	0.0	0.0	0.0
Transcription regulator activity	43	11	8.4	0.382	0.0	0.0	0.0	0.0
RNA polymerase II transcription factor activity	12	2	2.3	0.633	0.3	0.3	0.3	0.3
RNA polymerase III transcription factor activity	1	2	0.2	0.404	0.0	0.0	0.0	0.0
Transcription cofactor activity	9	2	1.7	0.616	0.0	0.0	0.0	0.0
Transcription factor activity	25	6	4.9	0.584	0.2	0.2	0.2	0.2
Transcriptional activator activity	4	1	0.8	0.575	0.6	0.6	0.6	0.6
Transcriptional repressor activity	4	2	0.8	0.346	0.1	0.1	0.1	0.1
Transcription initiation factor activity					0.1	0.1	0.1	0.1
Transcription termination factor activity					0.1	0.1	0.1	0.1
Structural molecule activity	99	10	19.2	0.041	2	2	2.4	2
Extracellular matrix structural constituent	4	2	0.8	0.346	1	1	0.1	0.1
Structural constituent of bone	1	1	0.2	0.404	0.0	0.0	0.0	0.0
Structural constituent of cytoskeleton	10	1	1.9	0.573	0.2	0.2	0.2	0.2
Structural constituent of muscle	1	1	0.2	0.404	0.0	0.0	0.0	0.0
Structural constituent of ribosome	70	5	13.6	0.025	1	1	1.7	1.7
Translation regulator activity	28	6	5.4	0.642	0.7	0.7	0.7	0.7
Translation factor activity, nucleic acid binding	28	6	5.4	0.642	0.7	0.7	0.7	0.7
Chaperone regulator activity	4	1	0.8	0.575	0.1	0.1	0.1	0.1
Antioxidant activity	4	1	0.8	0.575	0.1	0.1	0.1	0.1
Peroxidase activity	13	2	2.5	0.642	0.3	0.3	0.3	0.3
Molecular function unknown	7	1	1.4	0.631	0.2	0.2	0.2	0.2
Motor activity	2	2	0.4	0.619	0.0	0.0	0.0	0.0
Microtubule motor activity	2	2	0.4	0.619	0.0	0.0	0.0	0.0

Supplementary Table 3-1. continued

GO term	All			P < 0.05			P < 0.05		
	Number of clones in GO term	Number of clones in GO term	Expectation	Number of clones in GO term	Number of clones in GO term	Expectation	Number of clones in GO term	Number of clones in GO term	Expectation
All	1353	263	135.1	33	33	17.0	33	33	17.0
Biological process	695	141	135.1	141	141	135.1	141	141	135.1
Cellular process	618	129	120.1	129	129	120.1	129	129	120.1
Cell communication	276	53	53.6	53	53	53.6	53	53	53.6
Cell differentiation	93	23	18.1	23	23	18.1	23	23	18.1
Cellular physiological process	9	2	1.7	2	2	1.7	2	2	1.7
Membrane fusion	223	44	43.3	44	44	43.3	44	44	43.3
Regulation of cellular process	4	2	0.8	2	2	0.8	2	2	0.8
Physiological process	35	7	6.8	7	7	6.8	7	7	6.8
Cellular physiological process	570	113	110.8	113	113	110.8	113	113	110.8
Cellular physiological process	223	44	43.3	44	44	43.3	44	44	43.3
Coagulation	5	1	1.0	1	1	1.0	1	1	1.0
Death	11	2	2.1	2	2	2.1	2	2	2.1
Homeostasis	6	2	1.2	2	2	1.2	2	2	1.2
Metabolism	448	90	87.1	90	90	87.1	90	90	87.1
Organismal physiological process	40	12	7.8	12	12	7.8	12	12	7.8
Pathogenesis	1	1	0.2	1	1	0.2	1	1	0.2
Regulation of physiological process	83	20	16.1	20	20	16.1	20	20	16.1
Response to stimulus	62	19	12.1	19	19	12.1	19	19	12.1
Secretion	10	3	1.9	3	3	1.9	3	3	1.9
Biological process unknown	66	23	12.8	23	23	12.8	23	23	12.8
Development	1	1	0.2	1	1	0.2	1	1	0.2
Aging	9	2	1.7	2	2	1.7	2	2	1.7
Cell differentiation	1	1	0.2	1	1	0.2	1	1	0.2
Embryonic development	1	1	0.2	1	1	0.2	1	1	0.2
Genetic transfer	9	2	1.7	2	2	1.7	2	2	1.7
Growth	2	2	0.4	2	2	0.4	2	2	0.4
Mesoderm development	52	19	10.1	19	19	10.1	19	19	10.1
Morphogenesis	1	1	0.2	1	1	0.2	1	1	0.2
Pattern specification	2	2	0.4	2	2	0.4	2	2	0.4
Pigmentation	6	2	1.2	2	2	1.2	2	2	1.2
Regulation of development	9	2	1.7	2	2	1.7	2	2	1.7
Regulation of gene expression, epigenetic	9	4	1.7	4	4	1.7	4	4	1.7
Reproduction	111	25	21.6	25	25	21.6	25	25	21.6
Sex determination	35	7	6.8	7	7	6.8	7	7	6.8
Sex differentiation	6	2	1.2	2	2	1.2	2	2	1.2
Regulation of biological process	5	2	1.0	2	2	1.0	2	2	1.0
Regulation of cellular process	83	20	16.1	20	20	16.1	20	20	16.1
Regulation of development	1	1	0.2	1	1	0.2	1	1	0.2
Regulation of gene expression, epigenetic	1	1	0.2	1	1	0.2	1	1	0.2
Regulation of physiological process	1	1	0.2	1	1	0.2	1	1	0.2
Behavior	1	1	0.2	1	1	0.2	1	1	0.2
Feeding behavior	1	1	0.2	1	1	0.2	1	1	0.2
Learning and/or memory	1	1	0.2	1	1	0.2	1	1	0.2
Mechanosensory behavior	1	1	0.2	1	1	0.2	1	1	0.2
Viral life cycle	1	1	0.2	1	1	0.2	1	1	0.2
Viral infectious cycle	1	1	0.2	1	1	0.2	1	1	0.2

Supplementary Table 3-1. continued

GO term	All						P < 0.05			P < 0.05				
	Number of clones		Number of clones in		Expectation		P		Number of clones in		Expectation		P	
	GO term	GO term	GO term	GO term	GO term	GO term	GO term	GO term	GO term	GO term	GO term	GO term	GO term	GO term
All	1353	695	263	141	135.1	33	20	17.0	33	18	17.0	17.0	0.889	
Cellular component		564		112	109.6		16	13.8		14	13.8	13.8	0.481	
Cell		533		103	103.6		13	13.0		10	13.0	13.0	0.648	
Cell fraction		43		8	8.4			1.0		1	1.0	1.0	0.002	
Cell projection		1		1	0.2			0.0		1	0.0	0.0	0.000	
Intracellular		473		92	91.9		13	11.5		8	11.5	11.5	0.367	
Membrane		161		24	31.3		2	3.9		2	3.9	3.9	0.465	
Extracellular		34		12	6.6		4	0.8		6	0.8	0.8	0.000	
Extracellular matrix		15		6	2.9		2	0.4		4	0.4	0.4	0.000	
Extracellular space		9		2	1.7		1	0.2		1	0.2	0.2	0.541	
Unlocalized		4			0.8			0.1			0.1	0.1	0.196	
cAMP-dependent protein kinase complex					0.4			0.0			0.0	0.0	0.041	
Ferritin complex		2			0.2			0.0			0.0	0.0	0.002	
Glycerol-3-phosphate dehydrogenase complex		1			0.2			0.0			0.0	0.0	0.002	
Protein kinase CK2 complex		1			0.2			0.0			0.0	0.0	0.002	
Protein serine/threonine phosphatase complex														
Ribonucleoside-diphosphate reductase complex														
Cellular component unknown		14			2.7		1	0.3			0.3	0.3	0.766	